



IFW16

RAW SEQUENCE LISTING

DATE: 07/25/2006

PATENT APPLICATION: US/10/791,791A

TIME: 11:20:25

Input Set : A:\476352US.APP

Output Set: N:\CRF4\07252006\J791791A.raw

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3 <110> APPLICANT: NAKAO, YOSHIHIRO
4     NAKAMURA, NORIHISA
5     KODAMA, YUKIKO
6     FUJIMURA, TOMOKO
7     ASHIKARI, TOSHIHIKO
9 <120> TITLE OF INVENTION: SCREENING METHODS FOR GENES OF BREWING YEAST
11 <130> FILE REFERENCE: 47635-0002-00-US
13 <140> CURRENT APPLICATION NUMBER: 10/791,791A
14 <141> CURRENT FILING DATE: 2004-03-04
16 <150> PRIOR APPLICATION NUMBER: JP 2003-057677
17 <151> PRIOR FILING DATE: 2003-03-04
19 <160> NUMBER OF SEQ ID NOS: 37
21 <170> SOFTWARE: PatentIn Ver. 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1377
25 <212> TYPE: DNA
26 <213> ORGANISM: Saccharomyces sp.
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30 gttatggggg tcggtatttc atcgaatatt ctgtacagct tcccgatatcc ggcgaggtgg 120
31 ctgaggatat gctcgtacat catgtttgcc attacatggt tgattttcat ctctgtacag 180
32 gcgctgcagc ttttgcacat ggtcatctat atcaaagaaa aaagcttttag agattacttc 240
33 aatgaatatt tcagaagtct gaagtacaat ttattttggg gtacttatcc catgggatta 300
34 gtaacaatca taaatttttt gggggcgctg tcacaaaaat ttaccacgac aagccctgcy 360
35 aatgccaaagc acttgatcat ttttgtttac gtcctgtggt ggtatgacct cgcggtttgt 420
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37 gttggaaatc actcttcata cagttcacga atggcttccg accacatgaa aagcgtactg 540
38 ttgctagata tcattccgct ggtcgttggt gcttcgagcg gtgggacatt tacaatgtca 600
39 aaaatattcg gtaccacttt tgataggaat attcaattgc taacactggt catctgtgcc 660
40 ctggtttggc tacacgctct tatatttgtc tttattctga ttacaatata cttctggaat 720
41 ctttacatca ataagatacc accaatgacg caggtaattta cgttggttctt ggtattgggg 780
42 ccattgggcc aaggaagttt tggatatttg ttgcttactg acaatataag aaagtatgta 840
43 gaaaaatact acccaaggga aaacatcacc atggaacaag aaataactaac cattatggtt 900
44 cgtggtggtt tcaagggttct gggcatgaca tttgcttttg cattaatcgc tatgggttac 960
45 ttctttacgg taatttccct tatctcgatt ttatcatact acaatgaaag agttgttgac 1020
46 aatgaaacag gcaaagtga aaggatctac actttccata aaggtttctg ggggatgact 1080
47 ttcccgatgg gtaccatgtc tttgggaaac gaggagctgt atctgcaata caaccagtat 1140
48 gttcccttat atgcattcag agtcatagct accatatatg gtggtatttg tgtttgctgg 1200
49 tcaatcttat gcctctcgtg cacgttgatg ggttacctga aaacgattct ccatgctgcc 1260
50 cgtaaaacctt cgtttttatc agaggaaggg acggagaaga ctgtcaattc tcctttcaac 1320
51 agcatcgaaa gtgtggagga atcaaaactcg gctatcgata gtacatatat aacataa 1377
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 609

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56 <212> TYPE: DNA

57 <213> ORGANISM: Saccharomyces sp.

59 <400> SEQUENCE: 2

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60 atggctacta atatcacttg gcatccaaat cttacctacg acgaacgtaa ggaattaaga 60
61 aagcaagacg gctgtaccgt ttgggtgacc ggtctaagtg cgtcaggaaa aagtacaata 120
62 gcttgtgcac tggaacaatt actgcttcaa aaaaacttat ctgcttatag gtttagatggt 180
63 gataacattc gtttttggtt gaataaggat ttgggcttct cagaaaagga cagaaatgaa 240
64 aacattcgta gaattagtga agtatccaag ctattcgctg attcgtgtgc tgtatccatc 300
65 acttcattta tttccccata cagagtcgat agagacagag cccgtgattt acataaggaa 360
66 gcaggcttga agttcattga aatttttggt gatgttccat tagaagtcgc tgagcaaaga 420
67 gaccctaagg gtttgtataa gaaagccaga gaaggtgtga ttaaagagtt cactggtatt 480
68 tcagctcctt acgaagctcc aaaggcccca gagttgcatt taagaactga ccaaagact 540
69 gttgaagaat gtgctgctat catttatgag tacctggtca atgagaagat tatccggaag 600
70 catctataa                                     609

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73 <210> SEQ ID NO: 3

74 <211> LENGTH: 458

75 <212> TYPE: PRT

76 <213> ORGANISM: Saccharomyces sp.

78 <400> SEQUENCE: 3

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79 Met Val Ala Ser Trp Met Leu Thr Ala Thr Arg Asp Phe Asn Pro Phe
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82 Met Phe Val Met Val Met Gly Val Gly Ile Ser Ser Asn Ile Leu Tyr
83           20           25           30
85 Ser Phe Pro Tyr Pro Ala Arg Trp Leu Arg Ile Cys Ser Thr Ile Met
86           35           40           45
88 Phe Ala Ile Thr Cys Leu Ile Phe Ile Ser Val Gln Ala Leu Gln Leu
89           50           55           60
91 Leu His Met Val Ile Tyr Ile Lys Glu Lys Ser Phe Arg Asp Tyr Phe
92           65           70           75           80
94 Asn Glu Tyr Phe Arg Ser Leu Lys Tyr Asn Leu Phe Trp Gly Thr Tyr
95           85           90           95
97 Pro Met Gly Leu Val Thr Ile Ile Asn Phe Leu Gly Ala Leu Ser Gln
98           100          105          110
100 Lys Phe Thr Thr Thr Ser Pro Ala Asn Ala Lys His Leu Ile Ile Phe
101           115          120          125
103 Val Tyr Val Leu Trp Trp Tyr Asp Leu Ala Val Cys Leu Val Thr Ala
104           130          135          140
106 Trp Gly Ile Ser Phe Leu Ile Trp Gln Lys Tyr Tyr Phe Val Asp Gly
107          145          150          155          160
109 Val Gly Asn His Ser Ser Tyr Ser Ser Arg Met Ala Ser Asp His Met
110           165          170          175
112 Lys Ser Val Leu Leu Leu Asp Ile Ile Pro Leu Val Val Val Ala Ser
113           180          185          190
115 Ser Gly Gly Thr Phe Thr Met Ser Lys Ile Phe Gly Thr Thr Phe Asp
116           195          200          205
118 Arg Asn Ile Gln Leu Leu Thr Leu Val Ile Cys Ala Leu Val Trp Leu
119           210          215          220
121 His Ala Leu Ile Phe Val Phe Ile Leu Ile Thr Ile Tyr Phe Trp Asn
122          225          230          235          240

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124 Leu Tyr Ile Asn Lys Ile Pro Pro Met Thr Gln Val Phe Thr Leu Phe
125                245                250                255
127 Leu Val Leu Gly Pro Leu Gly Gln Gly Ser Phe Gly Ile Leu Leu Leu
128                260                265                270
130 Thr Asp Asn Ile Arg Lys Tyr Val Glu Lys Tyr Tyr Pro Arg Glu Asn
131                275                280                285
133 Ile Thr Met Glu Gln Glu Ile Leu Thr Ile Met Val Pro Trp Cys Phe
134                290                295                300
136 Lys Val Leu Gly Met Thr Phe Ala Leu Ala Leu Ile Ala Met Gly Tyr
137 305                310                315                320
139 Phe Phe Thr Val Ile Ser Leu Ile Ser Ile Leu Ser Tyr Tyr Asn Glu
140                325                330                335
142 Arg Val Val Asp Asn Glu Thr Gly Lys Val Lys Arg Ile Tyr Thr Phe
143                340                345                350
145 His Lys Gly Phe Trp Gly Met Thr Phe Pro Met Gly Thr Met Ser Leu
146                355                360                365
148 Gly Asn Glu Glu Leu Tyr Leu Gln Tyr Asn Gln Tyr Val Pro Leu Tyr
149                370                375                380
151 Ala Phe Arg Val Ile Ala Thr Ile Tyr Gly Gly Ile Cys Val Cys Trp
152 385                390                395                400
154 Ser Ile Leu Cys Leu Ser Cys Thr Leu Tyr Gly Tyr Leu Lys Thr Ile
155                405                410                415
157 Leu His Ala Ala Arg Lys Pro Ser Phe Leu Ser Glu Glu Gly Thr Glu
158                420                425                430
160 Lys Thr Val Asn Ser Pro Phe Asn Ser Ile Glu Ser Val Glu Glu Ser
161                435                440                445
163 Asn Ser Ala Ile Asp Ser Thr Tyr Leu Thr
164                450                455
167 <210> SEQ ID NO: 4
168 <211> LENGTH: 202
169 <212> TYPE: PRT
170 <213> ORGANISM: Saccharomyces sp.
172 <400> SEQUENCE: 4
173 Met Ala Thr Asn Ile Thr Trp His Pro Asn Leu Thr Tyr Asp Glu Arg
174 1                5                10                15
176 Lys Glu Leu Arg Lys Gln Asp Gly Cys Thr Val Trp Leu Thr Gly Leu
177                20                25                30
179 Ser Ala Ser Gly Lys Ser Thr Ile Ala Cys Ala Leu Glu Gln Leu Leu
180                35                40                45
182 Leu Gln Lys Asn Leu Ser Ala Tyr Arg Leu Asp Gly Asp Asn Ile Arg
183                50                55                60
185 Phe Gly Leu Asn Lys Asp Leu Gly Phe Ser Glu Lys Asp Arg Asn Glu
186 65                70                75                80
188 Asn Ile Arg Arg Ile Ser Glu Val Ser Lys Leu Phe Ala Asp Ser Cys
189                85                90                95
191 Ala Val Ser Ile Thr Ser Phe Ile Ser Pro Tyr Arg Val Asp Arg Asp
192                100                105                110
194 Arg Ala Arg Asp Leu His Lys Glu Ala Gly Leu Lys Phe Ile Glu Ile
195                115                120                125

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197 Phe Val Asp Val Pro Leu Glu Val Ala Glu Gln Arg Asp Pro Lys Gly
198      130                      135                      140
200 Leu Tyr Lys Lys Ala Arg Glu Gly Val Ile Lys Glu Phe Thr Gly Ile
201 145                      150                      155                      160
203 Ser Ala Pro Tyr Glu Ala Pro Lys Ala Pro Glu Leu His Leu Arg Thr
204                      165                      170                      175
206 Asp Gln Lys Thr Val Glu Glu Cys Ala Ala Ile Ile Tyr Glu Tyr Leu
207                      180                      185                      190
209 Val Asn Glu Lys Ile Ile Arg Lys His Leu
210      195                      200
213 <210> SEQ ID NO: 5
214 <211> LENGTH: 15
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
220      oligonucleotide
222 <400> SEQUENCE: 5
223 agtcacgacg ttgta                      15
226 <210> SEQ ID NO: 6
227 <211> LENGTH: 17
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
233      oligonucleotide
235 <400> SEQUENCE: 6
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239 <210> SEQ ID NO: 7
240 <211> LENGTH: 22
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
246      oligonucleotide
248 <400> SEQUENCE: 7
249 aggcgtatca cgaggccctt tc                      22
252 <210> SEQ ID NO: 8
253 <211> LENGTH: 29
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
259      oligonucleotide
261 <400> SEQUENCE: 8
262 cttatcgatg ataagcggtc aaacatgag                      29
265 <210> SEQ ID NO: 9
266 <211> LENGTH: 36
267 <212> TYPE: DNA

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268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
272     oligonucleotide
274 <400> SEQUENCE: 9
275 cgcaagctcc gtacgttcaa cattcttatg aacggc          36
278 <210> SEQ ID NO: 10
279 <211> LENGTH: 36
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
285     oligonucleotide
287 <400> SEQUENCE: 10
288 gcatcatcgt cgtgatacctt ctttggcaaa tgcagg          36
291 <210> SEQ ID NO: 11
292 <211> LENGTH: 36
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
298     oligonucleotide
300 <400> SEQUENCE: 11
301 gcgggtatatt tgatggtaaaa tctacaagcc ctcggc          36
304 <210> SEQ ID NO: 12
305 <211> LENGTH: 35
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
311     oligonucleotide
313 <400> SEQUENCE: 12
314 cccagacaca gtttccagta tcatacctcgc agaac          35
317 <210> SEQ ID NO: 13
318 <211> LENGTH: 26
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
324     oligonucleotide
326 <400> SEQUENCE: 13
327 gagctcatgg tcgctagttg gatgct          26
330 <210> SEQ ID NO: 14
331 <211> LENGTH: 26
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
337     oligonucleotide

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VERIFICATION SUMMARY

DATE: 07/25/2006

PATENT APPLICATION: US/10/791,791A

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